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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Thu Oct 21 16:29:45 1999; MasPar time 4.57 Seconds 519.801 Million cell updates/sec

Description: Perfect Score: Title: >US-08-978-217-7 (1-84) from US08978217.pep 599

Sequence: 1 NCALEELRLVFGPLGDQLHA......ELLDDGQQASPYHPGSCGAG 84

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37. 1:swissprot

Statistics: Mean 41.198; Variance 80.907; scale 0.509

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222117 322222118 32210	Result
Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	Score
15.7 15.7 15.2 14.9 14.9 14.7 14.7 14.2 14.2 14.2 14.2 14.2 14.2 14.2 14.2	Query Match
174 277 277 2870 2870 395 9916 9916 9916 241 183 308 183 308 241 241 241 241 241 241 341 348 348 348 348 348 348 348 348	% Query Match Length
	DB .
GSPM_PSEAE Y021_SYNY3 YBBB_ECOLI SYAC_YEAST NDVB_RHIME APA4_MOUSE APA4_MOUSE APA4_MOUSE APA6_COLI RPEP_ALCEU RPEP_ARTSA APE_PIG SOOM_RABIT RMLA_STRMU NUZM_ANOGA NUZM_ANOGA NUZM_ANOGA NUZM_ANOGA NUZM_LATCH PARE_BACGU CULL_SCHOO CXYB_RABIT RMLA_STRMU CULL_SCHOO CXYB_RABIT	ID
GENERAL SECRETION PATH PUTATIVE PROTEASE SLRO HYPOTHETICAL 41.1 KD P ALANYL-TRNA SYNTHETASE 319 KD PROTEIN. APOLLPOPROTEIN A-IV PR PREPROTEIN TRANSLOCASE EUKARYOTIC INITIATION HYPOTHETICAL 21.5 KD P RIBULOSE-PHOSPHATE 3-E SPECTRIN ALPHA CHAIN, HYPOTHETICAL 20.1 KD P GLYCINE-RICH PROTEIN G APOLLPOPROTEIN E PRECU SUPEROXIDE DISMITASE I GLUCOSE-1-PHOSPHATE TH NADH-UBIQUINONE OXIDOR OXYSTEROL-BINDING PROT OXYSTEROL-BINDING PROT	Description
1.00e-01 3.43e-01 8.45e-01 1.52e+00 1.52e+00 1.52e+00 2.04e+00 2.04e+00 2.04e+00 3.63e+00 4.82e+00	Pred. No.

δÃ В

Query Match 16.4%; Score 98; DB 1; Length 174; Best Local Similarity 30.4%; Pred. No. 1.00e-01; Matches 17; Conservative 17; Mismatches 21; Indels

<u>.</u> Gaps

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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
82	82	82	82	82	82	82	82	82	83	83	83	83	83	84	84	84	84	84	84	84	85
13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.9	13.9	13.9	13.9	٠	14.0				14.0	14.0		14.2
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DDX8_SCHPO	ALKS_PSEOL	SPEA_ECOLI	MEND_HAEIN	NU2M_DROSI	NU2M_DROSE	SODM_MOUSE	SODM_HUMAN	VG17_BPPH2	DP27_CAEEL	EP15_HUMAN	NI80_YEAST	E1A_ADE40	YDHR_ECOLI	DDX8_HUMAN	DPO1_CHLAU	COTS_BACSU	NU2M_DROME	NU2M_DROYA	NU2M_DROMA	OX4L_RABIT	FSC1_MOUSE
PUTATIVE PRE-MRNA SPLI	REGULATORY PROTEIN ALK	BIOSYNTHETIC ARGININE	2-SUCCINYL-6-HYDROXY-2	NADH-UBIQUINONE OXIDOR	NADH-UBIQUINONE OXIDOR	SUPEROXIDE DISMUTASE [SUPEROXIDE DISMUTASE [EARLY PROTEIN GP17.	CHROMOSOME CONDENSATIO	EPIDERMAL GROWTH FACTO	NIP80 PROTEIN (NIP100	EARLY E1A 27 KD PROTEI	HYPOTHETICAL 11.3 KD P	PROBABLE ATP-DEPENDENT	DNA POLYMERASE I (EC 2	SPORE COAT PROTEIN S (NADH-UBIQUINONE OXIDOR	NADH-UBIQUINONE OXIDOR	NADH-UBIQUINONE OXIDOR	OX40 LIGAND (OX40L).	MAJOR FIBROUS SHEATH P
1.11e+01	1.11e+01	1.11e+01	1.11e+01	1.11e+01	1.11e+01	,1.11e+01	1.11e+01	1,11e+01	8.44e+00	8.44e+00	8.44e+00	8.44e+00	8.44e+00	6.39e+00	6.39e+00	6.39e+00	6.39e+00	6.39e+00	6.39e+00	6.39e+00	4.82e+00

ALIGNMENTS

DR DR	8888888	88888	RT RA	20005		RESULT ID G
EMBL; X56183; G45443; PIR; S12356; S12356. PIR; S21639; S21639. TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE. TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE. TRANSMEM 33 52 POTENTIAL. SEQUENCE 174 AA; 19265 MW; 2160BB8F CRC32;	inls Swiss-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS!- SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE)!- SIMILARITY: BELONGS TO THE EXEM/PULM/OUTM/XCPZ FAMILY.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 91092255. MILLOUX A., BALLY M., BALL G., AKRIM M., TOMMASSEN J., LAZDUNSKI A.; "Protein secretion in gram-negative bacteria: transport across the outer membrane involves common mechanisms in different bacteria."; EMBO J. 9:4333-4329(1990).	XCPZ. PSEUDOMONAS AERUGINOSA. BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP; PSEUDOMONAS	01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) GENERAL SECRETION PATHWAY PROTEIN M.	LT 1 SSPM_PSEAE STANDARD; PRT; 174 AA.

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Best Local :
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01-FEB-1994 (REL. 38
01-NOV-1997 (REL. 35
01-NOV-1997 (REL. 3
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01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
PUTATIVE PROTEASE S
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Q55682;
Q5-01-NOV-1997
                                                                                                                                                                                                                                             SEQUENCE FROM NO....
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RO
RILEY M., COLLADO-VIDES J., GLASNER F.D., RO
RILEY M., COLLADO-VIDES J., GLASNER F.D., GO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE OF 268-364 FROM N.A.
                                              ROBERTS D., FELEN E., ARAUJO R., APARICIO A
DUNCAN M., FEDERSPIEL N., HYMAN R., KALMAN
LEW H., LIN D., NAMATH A., OEFNER P. SCHRA
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ D
                                                                                                                                       SEQUENCE FROM N.A. STRAIN-K12 / MG1655;
                                                                                                                                                                                                             SCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BBB
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PFAM; PF01343; Peptidase_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUGIURA M., TABATA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96127529.
KANEKO T., TANAKA A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY U7.
                                                                                                                                                                                                        complete genome sequence NCE 277:1453-1474(1997).
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35,
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35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
SLR0021 (EC 3.4.-.-).
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                                                TO EMBL/GENBANK/DDBJ DATA BANKS
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, LAST ANNOTATION UPDATE)
PROTEIN IN RHSD-GCL INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 1;
Pred. No. 3.43e-01
9; Mismatches 1
                                                                                                                                                                                                                               of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBDIVISION;
                                                                   APARICIO A., CHUNG
R., KALMAN S., KOMP
R P., SCHRAMM S., D!
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92% of the genome.";
                                                                                                                                                                                                                               Escherichia
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                                                                                                                                                                                                                                                                                          C.K., MAYHEW G.F.,
                                                                     MP C.,
DAVIS
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                                                                     DAVIS
KURDI
R.W.;
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Best Local S
Matches 1
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P40825;
01-FEB-1995
01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
ALANYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1
LIGASE) (ALARS).
                                                                                 entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                              Chromosome I.";
YEAST 12:999-1004(1996).
                                                                                                                                                                                                                                                                          PARLE-MCDERMOTT A.G., HAND N.J., GOU
"Sequence of 29 kb around the PDR10
Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
RIPMASTER T.L., SCHIMMEL P.;
SUBMITTED (DEC-1994) TO EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGASE) (ALARS).
ALA1 OR YOR335C.
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SADOSKY A.B., GRAY J.A., HILL C.W.;

"The Rhsp.c subfamily of Escherichia NUCLEIC ACIDS RES. 19:7177-7183(1991)
             EMBL; U18672; G609338; -.
EMBL; Z49821; E218690; -.
EMBL; Z75243; E252159; -.
SGD; L0002757; ALA1.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 97051586.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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NP_BIND 149 156 ATP (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 39.4%;
nes 13; Conservative
                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + L-ALANINE
PYROPHOSPHATE + L-ALANYL-TRNA(ALA).
SUBCELLULAR LOCATION: CYTOPLASMIC.
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                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
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Pred. No. 3.43e-01
10; Mismatches
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DA776C59 CRC32;
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(EC 6.1.1
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AA_TRNA_LIGASE_II_1; FALSE_NEG

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01-OCT-1996
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The ndvB locus of Rhizobium meliloti encodes a 319 kDa
involved in the production of beta-(1-->2)-glucan.";
J. BIOL. CHEM. 265:2843-2851(1990).
-!- FUNCTION: INVOLVED IN THE PRODUCTION OF BETA-(1,2)-(
TI IS INVOLVED NOT ONLY IN INVASION BUT ALSO IN BAC:
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AMINOACYL-TRNA SYNTHETASE; PROTEIN BIOSYNTHESIS; LIGASE; ATP-BINDING CONFLICT 136 136 R -> S(IN REF. 1).

CONFLICT 465 467 KDQ -> RTK (IN REF. 1).

CONFLICT 840 841 FE -> LQ (IN REF. 1).

SEQUENCE 958 AA; 107277 MW; AE929944 CRC32;
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01-FEB-1991 (REL.
01-FEB-1994 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
PIR; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                        APA4_MOUSE
P06728;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE
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BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
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                   APOLIPOPROTEIN
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nes 11; Conser
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE SIMILARITY: TO A.TUMEFACIENS CHVB.
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                                       (REL.
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                   EL. 06, CREATED)
EL. 34, LAST SEQUENCE UPDATE)
EL. 37, LAST ANNOTATION UPDAT
A-IV PRECURSOR (APO-AIV).
                                                                                                                            STANDARD;
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17, LAST SEQUENCE UPDATE)
28, LAST ANNOTATION UPDATE)
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KDQ -> RTK (IN REF. 1).

FE -> LQ (IN REF. 1).

MW; AE929944 CRC32;
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                                                                                                                                                                                                                                                                                         Score 91; DB 1;
Pred. No. 8.45e-01
8; Mismatches 1
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Pred. No. 8.45e-01;
17; Mismatches 16
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ALSO IN BACTEROID
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EMBL; M64249; G191887; -.
EMBL; M64248; G191885; -.
PIR; A25281; A25281.
MGD; MGI:88051; APOA4.
                                                                                                                                                                                                                                                                                         POLYMORPHISM.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by a high-lipid diet.";
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KINNIBURGH A.J.;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
TORMUTA- SCIUROGNATHI; MURIDAE; MURINAE;
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SUBMITTED (
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WILLIAMS S.C., BRI
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                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G., DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A., SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J. KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK KHALAK H., RICHARDSON D., HOWELL J.K., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., UTTERBACK M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAN M., MCLONALD M.D., FUJII C., GARLAN M., M., MCLONALD M.D., FUJII C., GARLAN M., MCLONALD M.D., FUJII C., GARLAN M.D., M.D., FUJII C., GARLAN M.D., M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREPROTEIN TRANSLOCASE SECA SUBUNIT SECA OR TP0379.
                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECA_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TREPONEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                    PROTEIN TRANSPORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 LEGEROGLGPNSGEVESHLSFLEKSLREKVNSFMSTLEKKGSPDQPQAL-PLP-EQAQEQ 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SECE SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO THE TRANSFER OF PRE-SECH PERIPELASMIC AND OUTER MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).

SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SECA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF
                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
23; Conse
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                                                        916 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of Treponema
                                                                              ATP-BINDING; MEMBRANE; TRANSLOCATION; 110 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389
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         14.9%;
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Pred. No.
20; Misma
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MISSING (IN REF. 1).
MISSING (IN REF. 1).
Q -> K (IN REF. 1).
E -> R (IN REF. 1).
S -> A (IN REF. 1).
RQ -> KA (IN REF. 1).
RQ -> KA (IN REF. 1).
RQ -> KA (IN REF. 1).
RX -> GG (IN REF. 1).
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                                                     84D5AFAC CRC32;
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         ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     916 AA
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       DB 1;
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    Length 916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMA MEMBRANE
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P39935;
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Best Local Similarity 34.2%;
Matches 13; Conservative
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
EUKARYOTIC INITIATION FACTOR 4F SUBUNIT P150
BINDING PROTEIN COMPLEX SUBUNIT P150).
TIF4631 OR YGR162W.
SACCHARDOWYNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOOLFORD J.L., TRACHSEL H., SONENBERG N.;
"TIF4631 and TIF4632: two yeast genes encoding the
"TIF4631 and TIF4632: two yeast genes encoding the
high-molecular-weight subunits of the cap-binding protein cor
(eukaryotic initiation factor 4F) contain an RNA recognition
motif-like sequence and carry out an essential function.";
MOL. CELL. BIOL. 13:4860-4874(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L16923; G295675; -. EMBL; Z72947; E243549; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                SGD; L0002309; TIF4631.
PROSITE; PS00030; RNP_1; FALSE_NEGINITIATION FACTOR; PROTEIN BIOSYNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of 20 chromosome VII."; YEAST 13:1077-1090(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOYER C., ALTMANN M., WOOLFORD J.L., TRACHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: INTERACTS WITH THE MRNA CAP STRUCTURE, M7GPPPX. THIS INTERACTION IS REQUIRED FOR EFFICIENT RIBOSOME BINDING TO THE MRNA. TIF4631 IS PROBABLY ESSENTIAL WHEN TIF4632 IS MISSING. SUBUNIT: THE CAP-BINDING PROTEIN COMPLEX IS COMPOSED OF AT LEAST TWO PROTEINS, A 24 KD (TIF45) AND A 150-200 KD SUBUNIT (TIF4631). SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
                                                                                                                                                                                                                                                                                                                                                                                                         A48086; A48086
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EL H., SONENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHAEFER M., MUELLER-AUER S.; kilobases from Saccharomyces
                                                                                                                                                                                                                                                                                                                                   BIOSYNTHESIS;
                 RNA-BINDING
RNA-BINDING
H -> Q (IN R)
T -> N (IN R)
Q -> K (IN R)
R -> K (IN R)
C -> E (IN R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agreement (See http://www.isb-sib.ch/announce/
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11; Mismatches 12;
                                                                                                                                                                                          POLY-GLU
                                                                                                                                                                                                              ARG/SER-RICH.
                                                                                                                                                                                                                                    ALA/GLU-RICH.
ARG/SER-RICH.
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    JUNDING (RNP2) (I
ADING (RNP1) (
ADING (RNP1) (
O (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                     RNA-BINDING;
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                                                                                                                                        (BY SIMILARITY). (BY SIMILARITY).
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P2553;
O1-MAY-1992 (REL. 2
O1-MAY-1992 (REL. 2
O1-NOV-1997 (REL. 2
HYPOTHETICAL 21.5 F
RPEP_ALCEU
Q04539;
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-K12 / MG1655;

MEDLINE; 97426617.

BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T.

RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., M.

RREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A.,

MENTER M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., M.

REGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A.,
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000374; G1789276; PIR; JQ0842; JQ0842. PIR; A47020; A47020. ECOGENE; EG11323; YGFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKAHIGASHI K., MIYAMOTO K., NISHIMURA K., INOKUCHI H.; "ISOLATION and characterization of a light-sensitive mutant Escherichia coli K.12 with a mutation in a gene that is requthe biosynthesis of ubiquinone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAU B., SHAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-HB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: STRONG, TO H.INFLUENZAE H10817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESCHERICHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (F194).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772
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                                                                                                                                             MKDLTDSPSEETLESVVELLNTVGEQFETDSFRTGQATLEGSQLLDSLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D90281; G216626; -. U28377; G882439; -.
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                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93054351.
                                                                                                                                                                                                                                                                                                                                           194 AA;
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larity 32.7%;
Conservative
     (REL.
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174:7352-7359(1992).
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                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22, CREATED)
22, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
KD PROTEIN IN PEPP-SSR INTE
  31, CREATED
                                                                                                                                                                                                                                                                    14.7%;
                                                                                                                                                                                                                                                                                                                                           21474 MW;
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                                                                                                                                                                                                                                                                    Score 88;
Pred. No.
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15; 1
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Pred. No. 1.52e+00;
                                                                                                                                                                                                                                                16;
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                                                     PRT;
                                                                                                                                                                                                                                                                                                                                             104C05A8 CRC32;
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                                                  241
                                                                                                                                                                                                                                                                    DB 1; I
2.04e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                                                                                                                                           Length 194;
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Best Local S
Matches 1
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PROSITE; PS01085; RIBUL_P_3_EPIMER_1; 1.

PROSITE; PS01086; RIBUL_P_3_EPIMER_2; 1.

PFAM; PF00834; Ribul_P_3_epim; 1.

PFAM; PF00834; Ribul_P_3_epim; 1.

TSOMERASE; CARBOHYDRATE METABOLISM; CALVIN CYCLE;

TSOMERASE; CARBOHYDRATE METABOLISM; CALVIN CYCLE;
MEDLINE: 90009318.

SAHR K.E., TOBE T., SCARPA A., LAUGHINGHOUSE K., MARCHESI S.L.,

AGRE P., LINNENBACH A.J., MARCHESI V.T., FORGET B.G.;

AGRE P., LINNENBACH A.J., MARCHESI V.T., FORGET B.G.;

"Sequence and exon-intron organization of the DNA encoding the alpha

"Gomain of human spectrin. Application to the study of mutations
                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
SAHR K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPCA_HUMAN STANDARD; PRT; 2418 AA. P02549; Q15514; CREATED) C1-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) C1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The Calvin cycle enzyme pentose-5-phosphate 3-epimerase within the cfx operons of the chemoautotroph Alcaligenes J. BACTERIOL. 174:7337-7344(1992).

-i- CATALYTIC ACTIVITY: D-RIBULOSE 5-PHOSPHATE - D-XYLULO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
RIBULOSE-PHOSPHATE 3-EPIMERASE, PLASMID (EC 5
PHOSPHATE 3-EPIMERASE) (PPE) (R5P3E).
                                                                                                                                                                                                                                            "The complete cDNA and alpha-spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECTRIN ALPHA CHAIN,
SPTA1 OR SPTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-H16 / ATCC 17699;
MEDLINE; 93054349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CBBEP OR CFXE.
                                                                                                            SEQUENCE OF 1-533 MEDLINE; 90009318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLASMID MEGAPLASMID PHG1.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                    CURTIS P.J., FORGET
                                                                                                                                                                                                                                                                                                                        SAHR K.E., LAURILA P., KOTULA L.,
LINNENBACH A.J., WINKELMANN J.C.,
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 90170949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RALSTONIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALCALIGENES EUTROPHUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 LVLNPATPLSWLDHTLDKLDLVLLMSVNPG-FG-GQAFIPGVLDKVRQA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                        BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTSSSSDELSWIIELLEKDGMAFQEALDPGPFDQGSPFAQELLDDGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 14.7%;
Similarity 30.6%;
15; Conservative
                                                                                                                                                                                                                     CHEM. 265:4434-4443(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALVIN CYCLE
                                                                                                                                                                    FROM
                                                                                                                                                                                                                                                                                                    B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERYTHROCYTE.
                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                           polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO THE RIBULOSE-PHOSPHATE 3-EPIMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA SUBDIVISION; BURKHOLDERIA GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
13; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMOH
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                                                                                                                                                                                                                                                                                                                           SCARPA A.L., CO
SPEICHER D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.04e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
                                                                                                                                                                                                                                                                                                                                                          COUPAL E.,
                                                                                                                                                                                                                                                                        human erythroid
                                                                                                                                                                                                                                                                                                                                 MARCHESI V.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-XYLULOSE
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                                                                                                                                                                                                                                                                                                                                                          LETO T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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MEDLINE: 84087887.

MEDLINE: 84087887.

SPEICHER D.W., DAVIS G., YURCHENCO P.D., MARCHESI V.T.;

Structure of human erythrocyte spectrin. I. Isolation of the common and its cyanogen bromide peptides.";

J. BIOL. CHEM. 258:14931-14937(1983).
                                                                                                                                                                                                                                MAILLET P., ALLOISIO
                                                                                                                                                                                                                                                                                                  segments.";
NATURE 311:177-180(1984).
                                                                                                                                                                                                                                                                                                                                                                    SAHR K.E., TOBE T., SCARPA A.L., LAUGHINGHOUSE K., MARCHESI AGRE P., LINENBACH A.J., MARCHESI V.T., FORGET B.G.; "Sequence and exon-intron organization of the DNA encoding I domain of human spectrin. Application to the study of mut causing hereditary elliptocytosis."; J. CLIN. INVEST. 84:1243-1252(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 7-601
MEDLINE; 84087888.
SPEICHER D.W., DAVIS G., MARCHES
"Structure of human erythrocyte
alpha-I domain ;
J. BIOL. CHEM. 258:14938-14947(1)
                                           COETZER T.L., SAHR K., PRCHAL J., BLACKLOCK H. DOYLE J., MANASTER J., PALEK J.;

"Four different mutations in codon 28 of alphe associated with structurally and functionally I/74 in hereditary elliptocytosis.";

J. CLIN. INVEST. 88:743-749(1991).
                                                                                                                          hereditary elliptocytosis: further support for folding unit model of the spectrin heterodimer BLOOD 84:303-308(1994).
                                                                                                                                                  PARQUET N., DEVAUX I., BOULANGER L., GALAND C. LECOMTE M.-C., DHERMY D., GARBARZ M.; "Identification of three novel spectrin alpha"
                                                                                                                                                                                                         spherocytosis.";
HUM. MUTAT. 8:97-107(1996).
                                                                                                                                                                                                                                                                                IDENTIFICATION GIBSON T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 7-533
MEDLINE; 90009318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINNENBACH A.J., SPEICHER D.W., MARCHESI V.T., FOR "Cloning of a portion of the chromosomal gene for alpha-specturin by using a synthetic gene fragment, PROC. NATL. ACAD. SCI. U.S.A. 83:2397-2401(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 causing
         MEDLINE; 91:
FLOYD P.B.,
                                                                                                                                                                                                                                                                                                                     "Erythrocyte spectrin
                                                                                                                                                                                                                                                                                                                                   MEDLINE; 84295638.
SPEICHER D.W., MARCHESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 320-45
MEDLINE; 86205962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF MEDLINE; 840
                                                                                                                                                                                                                            "Spectrin mutations
                                                                                                                                                                                                                                                     REVIEW ON VARIANTS.
                                                                                                                                                                                                                                                                       UNPUBLISHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hereditary elliptocytosis.";
. INVEST. 84:1243-1252(1989).
                                                                                                91358728; H
                                                                                                                                                                               94289716.
                                                                                                                                                                                                                                                                                                                                                                                                                       90009318.
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                                                                                                                                                                                                                                                                       OBSERVATIONS
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          GALLAGHER
                                                                                                                                                                                                                                                                                       ç
                           AND
                                                                                                          HIS-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.,
                                                                                                                                                                                                                                                                                        PROBABLE
                           ARG-48
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                                                                                                           LEU-28
                                                                                                                                                                                                                                                                      (MAR-1995)
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hrocyte spectrin.
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ZARKOWSKY H.S.,
                                                            VARIANT JENDOUBA.
MEDLINE; 92345619.
ALLOISIO N., WILMO
                                                                                                                                                                                                                                                                                                                 VARIANT BARCELONA. MEDLINE; 93372367.
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                                            DELAUNAY J.;
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          80:809-815(1992).
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Spectrin repeat 17 that severily spectrin repeat the erythrocyte spectrin association of the erythrocyte spectrin BIOL. CHEM. 268:22656-22662(1993).
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WILMOTTE R., MARECHAL J., MORLE L., BAKLOUTI F., PHI WILMOTTE R., MARECHAL J., DELAUNAY J., ALLOISIO N.; "LOW expression allele alpha LELY of red cell spectr with mutations in exon 40 (alpha V/41 polymorphism) with partial skipping of exon 46."; J. CLIN. INVEST. 91:2091-2096(1993).
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"Spectrin Jendouba: an alpha II associated with elliptocytosis the dimer self-association site
                                                                                                                                                                                                                                                                                      MORLE L., ROUX A.-F., ALLOISIO N., POTHIER B., STARCK J., DENOR MORLE F., RUDIGOZ R.-C., FORGET B.G., DELAUNAY J., GODET J.; MORLE F., RUDIGOZ R.-C., FORGET B.G., DELAUNAY J., GODET J.; Two elliptocytogenic alpha I/74 variants of the spectrin alpha domain. Spectrin Culoz (GGT--SGTT; alpha I 40 Gly-->Val) and spectrin Lyon (CTT-->TTT; alpha I 43 Leu-->Phe)."; J. CLIN. INVEST. 86:548-554(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS CULOZ AND LYON. MEDLINE; 90347052.
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                                                                                                                         ALLOISIO N., WILMOTTE R., DUCLUZEAU M.-T., DENOROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Spectrin Cagliari:
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M.-C., GARBARZ M.,
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BARUCHEL !
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that severely disrupts the structure
erythrocyte spectrin heterodimer.";
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A., BALLAS S.K., DHERMY
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"Spectrin Tunis (Sp alpha I/78), an elliptocytogenic variant, to the CGG-->TGG codon change (Arg-->Trp) at position 35 of the alpha I domain.";
                                                                                                                                                            STRAIN-K12 / MG1655;

MEDLINE: 97426617.

BLATTNER F.R., PLUNKETT G. III, BLOCH C.!

RILEY M., COLLADO-VIDES J., GLASNER F.D.,

RREGOR J., DAVIS N.W., KIRKPATRICK H.A.,
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P24250;
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"Spectrin Anastasia (alpha 1/78): a new spectrin variant (alpha 45 Arg-->Thr) with moderate elliptocytogenic potential.";

BR. J. HAEMATOL. 89:933-936(1995).

-!- FUNCTION: SPECTRIN IS THE ENTHAPOR CONSTITUENT OF THE CYTOSKELETAL NETWORK UNDERLYING THE ENTHAPORTE PLASMA MEMBRANE. IT ASSOCIATES WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF THE ERYTHROCYTE PLASMA MEMBRANE.
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MEDLINE; 89323436.
MORLE F.,
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MEDLINE; 94250920
                         STRAIN-K12
                                             SEQUENCE FROM N.A
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Local Similarity 31.3%;
hes 15; Conservative
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                                                                                                                                           B., SHAO Y.;
                                                                                           complete genome sequence of 
NCE 277:1453-1474(1997).
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173:4983-4993(1991).
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EMBL; AE000271; G1788063; -
EMBL; D80820; G1742876; -.
PIR; A40360; A40360.
ECOGENE; EG11134; YDJA.
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRUZ-ALVAREZ M., PELLICER A.; "Cloning of a full-length complementary DNA for an glycine-rich protein. Structural relationship with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (REL. 13,
01-JAN-1990 (REL. 13,
01-NOV-1997 (REL. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                          EMBL; J03453; G161174; -. PIR; A29379; A29379. NUCLEAR PROTEIN; RIBONUCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCINE-RICH PROTEIN GRP33.
ARTEMIA SALINA (BRINE SHRIMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECOGENE; EG11134; YDJA. PFAM; PF00881; Nitroreductase; HYPOTHETICAL PROTEIN.
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- PIM: THE ARCININES IN THE GLY-RICH DOMAIN MIGHT BE-
- SIMILARITY: TO HD40, THE MAJOR PROTEIN COMPONENT O
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN PARTICLES,
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SIMILARITY: STRONG, TO H.INFLUENZAE HI1542.
                                                                                                                                                                                                                                                                                                                                                            STRUCTURALLY TO OTHER NUCLEAR RNA BINDING PROTEINS.
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                             RIBONUCLEOPROTEIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEISGRABER K.H., TROXLER R.F., RALL S.C., MAHLEY R.W.;
"Comparison of the human, canine and swine E apoproteins.";
BIOCHEM. BIOPHYS. RES. COMMUN. 95:374-380(1980).
-i- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAMSOONDAR J.J., RUCKER E.B., VAZQUEZ J.C. SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ
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                            REPEAT
                                                                                                                                                                                                                                                                                                                         GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMNANT) OF HEPATIC TISSUES.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: SECRETED IN PLASMA.
-!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 /
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S33450; S33450.
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PROTEIN; PLASMA; LIPID TRANSPORT; HDL;
                                                                                                                                                                                                                                                                                                     BINDING;
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Pred. No. 3.63e+00
                                                                                                                                            APOLIPOPROTEIN E.
LDL RECEPTOR BINDING (POTENTIAL).
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
8 X 22 AA APPROXIMATE TANDEM REPEATS.
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DATA BANKS.
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P41982;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UP
01-FEB-1996 (REL. 33, LAST ANNOTATION
SUPEROXIDE DISMUTASE [MN] PRECURSOR (E
                                                                                                                                                                                                        modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORYCTOLAGUS CUNICULUS (RABBIT). EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                         PFAM; PF00081; sodfe;
HSSP; P04179; 1MSD.
                                                                                                                                                                                    EMBL; L28808; G454175; -.
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-NEW ZEALAND WHITE;
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FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.

CAPALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).

SUBGULT: HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE
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                       MITOCHONDRION (BY SIMILARITY).
SUPEROXIDE DISMUTASE, MANGANESE
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
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3CBFFC2E CRC32;
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(EC 1.15.1.1) (FRAGMENT).
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3.63e+00;
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MBL outstation -
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Matches 1
                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.
RILEY M., COLLADO-VIDES J., GLASNER F.D.
GREGOR J., DAVIS N.W., KIRKPATRICK H.A.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P24250,
01-MAR-1992 (REL. 2.
01-MAR-1992 (REL. 2.
01-NOV-1997 (REL. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1318
                                                                                                                                                                                                                                                                                                                       SAWERS G., HEIDER J., ZEHELEIN E., BOECK A.;
"Expression and operon structure of the sel genes and identification of a third selenium-containing dehydrogenase isoenzyme.";
J. BACTERIOL. 173:4983-4993(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDJA_ECOLI
P24250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arg-->Thr) with moderate elliptocytogenic potential.";
BR. J. HARMATOL. 89:933-936(1995).

-i- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL NETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF THE ERYTHROCYTE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94250920.

PERROTTA S., DEL GIUDICE E.M., ALLOISIO N
DELAUNAY J. CUTILLO S., LOLASCON A.;

"Mild elliptocytosis associated with the
in spectrin Genova (alpha 1/74).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MORLE L., MORLE F., ROUX A.F., GODET J., FORGET B.G., GARBARZ M., DHERMY D., KASTALLY R., DELAUNAY J.; "Spectrin Tunis (Sp alpha I/78), an elliptocytogenic v to the CGG-->TGG codon change (Arg-->Trp) at position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 95290423.
PERROTTA S., IOLASCON A., DE ANGELIS F.,
CUTILLO S., DEL GIUDICE E.M.;
"Spectrin Anastasia (alpha 1/78): a new."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 91317715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOOD 74:828-832(1989).
                                              SEQUENCE FROM N.A
                                                                                               SCIENCE
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MEDLINE; 89323436.
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                                                                                          complete genome sequence NCE 277:1453-1474(1997).
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                                                                                                                                                               KIRKPATRICK H.A.,
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Pred. No. 2.04e
15; Mismatches
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                                                                                                                     Escherichia coli K-12.";
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2.04e+00;
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01-JAN-1990
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                                     PIR; A29
NUCLEAR
                                                                                                                                                                                                                  modified
entities
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"Cloning of a full-length complementary DNA for an "Cloning of a full-length complementary DNA for an alveine-rich protein. Structural relationship with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYCINE-RICH PROTEIN GRP33.
ARTEMIA SALINA (BRINE SHRIMP).
EUKARYOTA; METAZOA; ARTHROPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRP3
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ITOH T., KASAI H., KASHIMOTO K., KIMURA S., KITAKAWA
KITACAWA M., MAKINO K., MIKI T., MIZOBUCHI K., MORI H
MOTOMURA K., NAKADE S., NAKAMURA Y., NASHIMOTO H., NI
OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAN
TAGAMI H., TAKEDA J., TAKEMOTO K., TAKEUCHI Y., WADA
YAMAMOTO Y., HORIUCHI T.;
                                                                       EMBL; J03453; G161174; -. PIR; A29379; A29379.
                                                                                                                                                                                                                                                                                                                           the
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proteins.";
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ECOGENE; EG11134; YDJA.
PFAM; PF00881; Nitroreductase;
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M68961; G147021; -. EMBL; AE000271; G1788063; -.
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-i- SIMILARITY: STRONG, TO H.INFLUENZAE HI1542.
                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOL. CHEM. 262:13377-13380(1987).
- PTM: THE ARGININES IN THE GLY-RICH DOMAIN MIGHT I
- SIMILARITY: TO HD40, THE MAJOR PROTEIN COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN PARTICLES, AND STRUCTURALLY TO OTHER NUCLEAR RNA BINDING PROTEINS.
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                                                                                                                                                                         non-profit institutions as long as its content is ind and this statement is not removed. Usage by and for content a license agreement (see http://www.isb-sib.ch) an email to license@isb-sib.ch).
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Similarity 26.98;
14; Conservative
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(REL. 13,
(REL. 35,
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Pred. No. 3.63e+00;
15; Mismatches 20
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MBL outstation -
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RIBONUCLEOPROTEIN; 118 KH.

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Best Local S
Matches 1
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01-NOV-1990 (REL. 16, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
APOLIPOPROTEIN E PRECURSOR (APO-E).
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EMBL; U70240; G2388609; ...
PIR; A05312; A05312.
PIR; S33450; S33450.
HSSP; P02649; 10EF.
GLYCOPROTEIN; PLASMA; LIPID TRANSPORT; HDL; VLDL;
HEPARIN-BINDING; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRZOZOWSKA A.M., GRIMHOLT U., KULSETH M.A SUBMITTED (MAY-1993) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
BRZOZOWSKA A.M.,
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                                                                                                                                                                     DOMAIN
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-!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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SUBCELLULAR LOCATION: EXTRACELLULAR.
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llarity 34.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TROXLER R.F., RALL S.C., MAHLEY R.W.; he human, canine and swine E apoproteins."; RES. COMMUN. 95:374-380(1980).
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RMES; SUINA;
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Pred. No. 3.63e+00;
14; Mismatches 15
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; 52ADC873 CRC32;
                                                                                                                   APOLIPOPROTEIN E.

LDL RECEPTOR BINDING (POTENTIAL).

HEPARIN-BINDING (BY SIMILARITY).

HEPARIN-BINDING (BY SIMILARITY).

8 X 22 AA APPROXIMATE TANDEM REPE
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A; SUIDAE; SUS.
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                                                                                                                                                                                                                                                                SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

1. FUNCTION: DESTROYS RADICALS WHICH ARE MORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.

1. CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).

1. SUBURLI: HOMOTETRAMER (BY SIMILARITY).

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1. SUBLELLULAR LOCATION: MITOCHONDRIAL MATRIX.
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-PEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.
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